

**SUBTRACTED
(Hypothalamus)**

0.8 ng
4 ng
20 ng
100 ng

NSE
Cyclophilin
POMC
Vasopressin
pT7T3D
PKC δ
GH

FIG. 1A

0.8 ng
4 ng
20 ng
100 ng

NSE
Cyclophilin
POMC
Vasopressin
pT7T3D
PKC δ
GH

TARGET
(Hypothalamus)

FIG. 1C

0.8 ng
4 ng
20 ng
100 ng

NSE
Cyclophilin
POMC
Vasopressin
pT7T3D
PKC δ
GH

DRIVER

FIG. 1B

(Cerebellum+ Hippocampus)

D1 D2 T

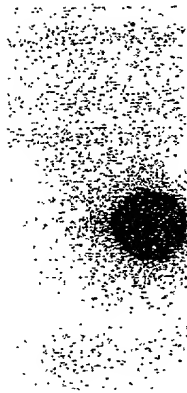


FIG. 2A

D1 D2 T

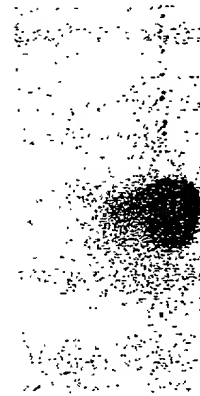


FIG. 2B

D1 D2 T



FIG. 2C

D1 D2 T



FIG. 2D

FIG. 3A

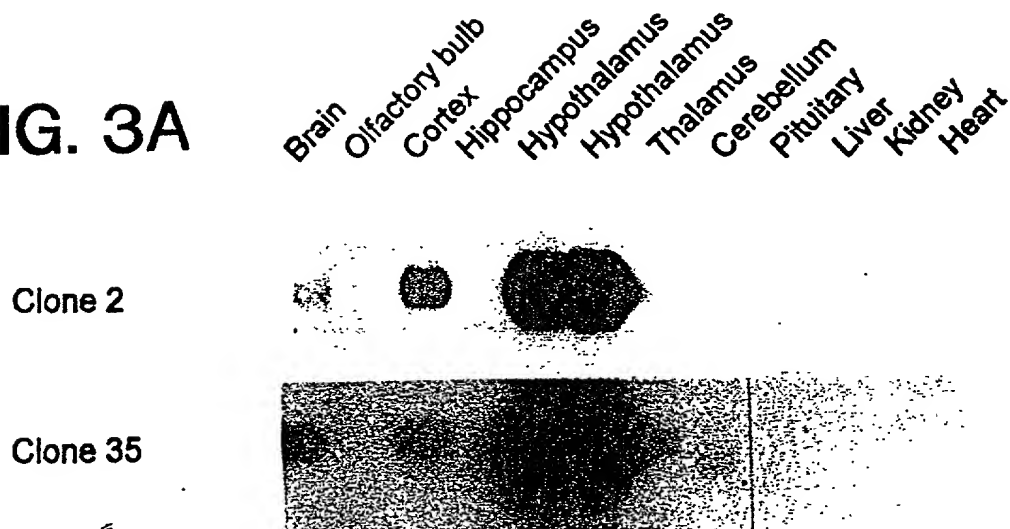
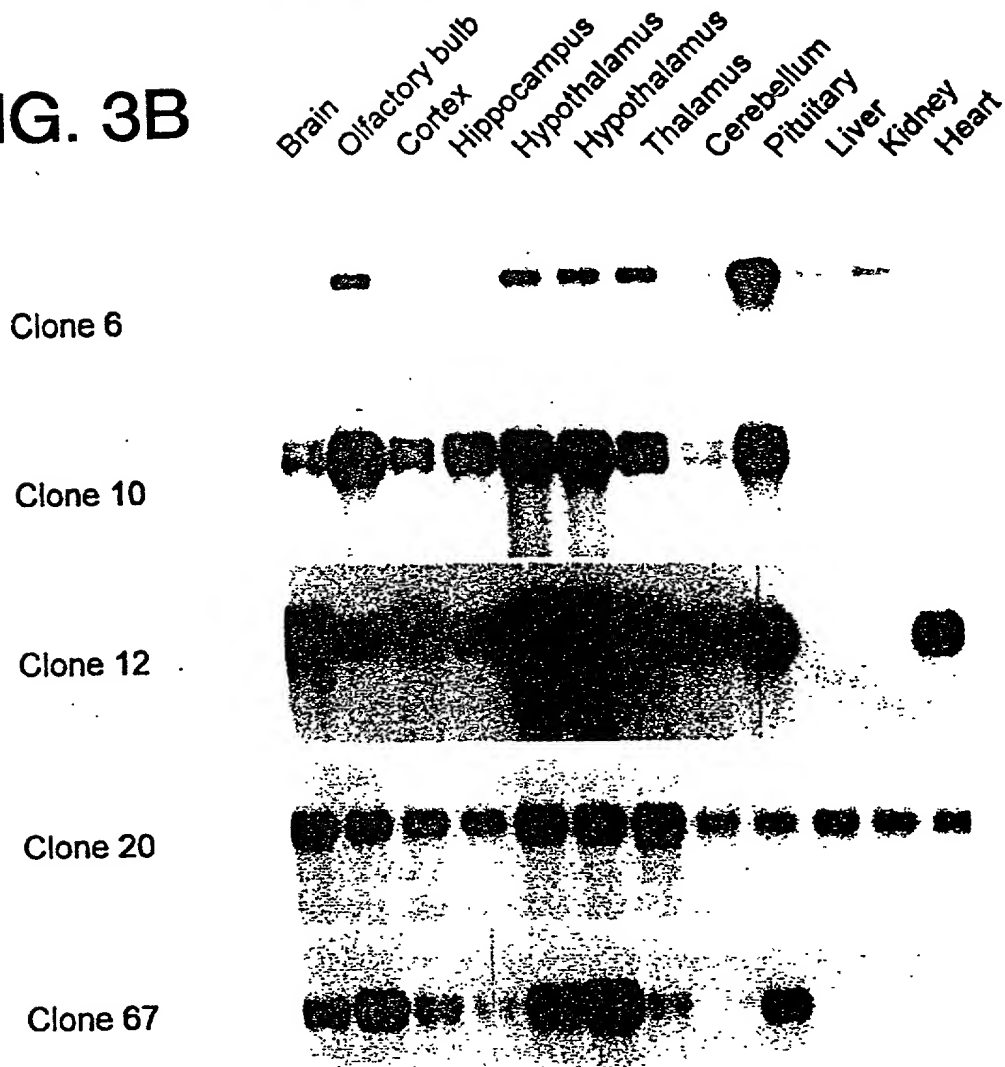


FIG. 3B



Brain
Olfactory bulb
Cortex
Hippocampus
Hypothalamus
Hypothalamus
Thalamus
Cerebellum
Pituitary
Liver
Kidney
Heart

Clone 3

Clone 15

Clone 29

FIG. 3D

Brain
Olfactory bulb
Cortex
Hippocampus
Hypothalamus
Hypothalamus
Thalamus
Cerebellum
Pituitary
Liver
Kidney
Heart

Clone 21

Clone 37

Clone 98

Clone 99

Cyclophilin

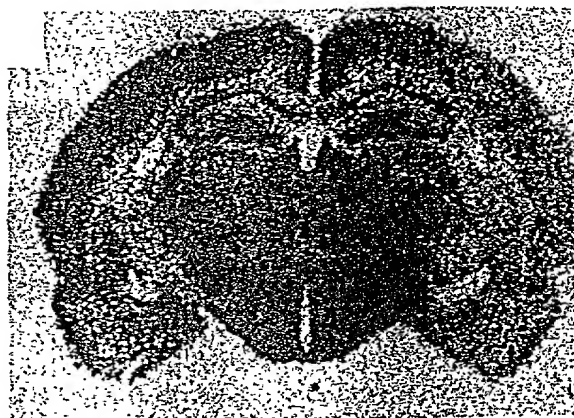


FIG. 4A

FIG. 4D

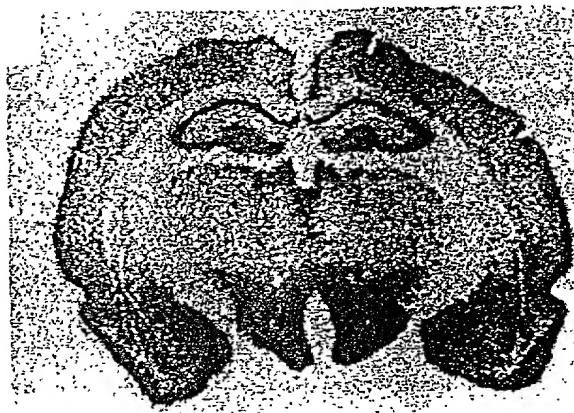
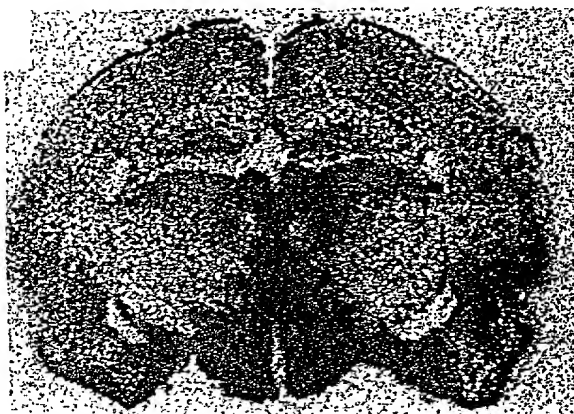


FIG. 4B

FIG. 4E

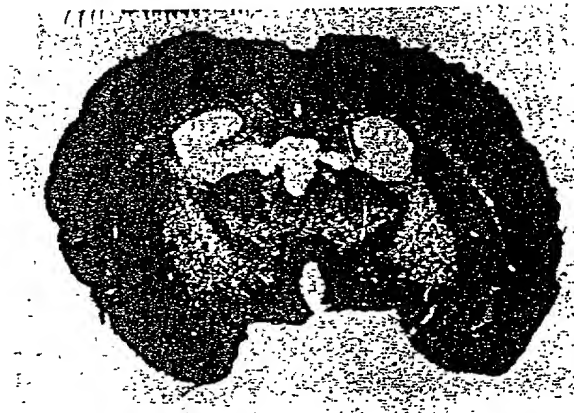
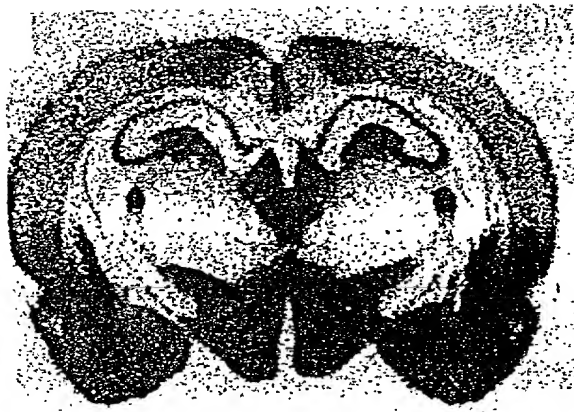


FIG. 4C

FIG. 4F

[illegible]

FIG. 5A

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M  N  L/F P  S  T  K  V  P  W  A  A  V  T  L  L
ATG AAC CTT CCT TCT ACA AAG GTT CCC TGG GCC GCC GTG ACG CTG CTG
ATG AAC TTT CCT TCT ACA AAG GTT CCC TGG GCC GCC GTG ACG CTG CTG
*
L  L  L  L  L  P  P  A  L  L  S  L  G  V  D  A
CTG CTG CTA CTG CTG CCG CCG GCG CTG CTG TCG CTT GGG GTG GAC GCG
CTG CTG CTA CTG CTG CCG CCG GCG CTG CTG TCG CTT GGG GTG GAC GCA
*
Q  P  L  P  D  C  C  R  Q  K  T  C  S  C  R  L
CAG CCT CTG CCC GAC TGC TGT CGC CAG AAG ACG TGT TCC TGC CGT CTC
CAG CCT CTG CCC GAC TGC TGT CGC CAG AAG ACG TGT TCC TGC CGT CTC
*
Y  E  L  L  H  G  A  G  N  H  A  A  G  I  L  T
TAC GAA CTG TTG CAC GGA GCT GGC AAC CAC GCC GCG GGC ATC CTC ACT
TAC GAA CTG TTG CAC GGA GCT GGC AAC CAC GCT GCG GGT ATC CTG ACT
*
L  G  K  R  R  P  G  P  P  G  L  Q  G  R  L  Q
CTG GGA AAG CGG CGA CCT GGA CCC CCA GGC CTC CAA GGA CGG CTG CAG
CTG GGA AAG CGG CGG CCT GGA CCT CCA GGC CTC CAG GGA CGG CTG CAG
*
R  L  L  Q  A  N  G  N  H  A  A  G  I  L  T  M
CGC CTC CTT CAG GCC AAC GGT AAC CAC GCA GCT GGC ATC CTG ACC ATG
CGC CTC CTT CAG GCC AAC GGT AAC CAC GCA GCT GGC ATC CTG ACC ATG
*
G  R  R  A  G  A  E  L  E  P  Y/H P  C  P/S G  R
GGC CGC CGC GCA GGC GCA GAG CTA GAG CCA TAT CCC TGC CCT GGT CGC
GGC CGC CGC GCA GGC GCA GAG CTA GAG CCA CAT CCC TGC TCT GGT CGC
*
R/G C  P  T  A/V T  A/T T  A  L  A  P  R  G  G  S
CGC TGT CCG ACT GCA ACC GCC ACC GCT TTA GCG CCC CGG GGC GGA TCC
GGC TGT CCG ACC GTA ACT ACC ACC GCT TTA GCA CCC CGG GGA GGG TCC
*
R/G V
AGA GTC TGA
GGA GTC TGA
*

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FIG. 5B

```

consensus:          RL  LL  GNHAAGILT G
hcrt1:             LGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
hcrt2:             PGPPGLQGRLLQRLQLQANGNHAAGILTMG
SECRETIN:         HSDGTFTSKLSRLRDSARLQRLQLGLV HSDGTFTSK
                   * * * * *

```

1 GCTAGGAGACATTGCGGCGGCGGTGGCGGCGTTGGCAGCAGCTGCAGACATGCTGCTGCT
-----+-----+-----+-----+-----+-----+ 60
CGATCCTCTGTAAACGCCGCCGCCACCGCCGCAACCGTCGTCGACGTCTGTACGACGACGA
M L L L

61 CAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGG
-----+-----+-----+-----+-----+-----+ 120
GTTCTTTGTCTGCCCTCCTGTAGTCGTACAGATACTCTAGGCCCTCTTCGACCCGAGCCC
K K Q T E D I S S V Y E I R E K L G S G

121 TGCCTTCTCTGAGGTGATGCTGGCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAA
-----+-----+-----+-----+-----+-----+ 180
ACGGAAGAGACTCCACTACGACCGGGTCCTTTCCCGAGACGAGTAGAACACCGGGAGTT
A F S E V M L A Q E R G S A H L V A L K

181 GTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCAGT
-----+-----+-----+-----+-----+-----+ 240
CACGTAAGGGTTCTTTTCGTGAAGCCCCGTTCCCTCCGGGACCACCTCTTACTCTAGCGTCA
C I P K K A L R G K E A L V E N E I A V

241 ACTCCGCAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGACGTCCACGAGAGCCCTTC
-----+-----+-----+-----+-----+-----+ 300
TGAGGCGTCTAATCGGTGGGGTTGTAACACCGAGACCTCCTGCAGGTGCTCTCGGGAAG
L R R I S H P N I V A L E D V H E S P S

301 CCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGTGTTGACCGAATCATGGA
-----+-----+-----+-----+-----+-----+ 360
GGTAGAGATGAACCGGTACCTCGACCATGTCCACCACTTGACAAACTGGCTTAGTACCT
H L Y L A M E L V T G G E L F D R I H E

361 GCGGGGCTCCTACACAGAGAAGGATGCGAGCCACCTTGTAGGGCAGGTCCTTGGTGCTGT
-----+-----+-----+-----+-----+-----+ 420
CGCCCCGAGGATGTGTCTCTTCTACGCTCGGTGGAACATCCCGTCCAGGAACCACGACA
R G S Y T E K D A S H L V G Q V L G A V

421 CTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTA
-----+-----+-----+-----+-----+-----+ 480
GAGGATGGAAGTATCGGACCCGTAGCACGTGGCCCTGGAGTTCGGACTTTTGGAGGAGAT
S Y L H S L G I V H R D L K P E N L L Y

481 TGCCACACCTTTTGGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATTCA
-----+-----+-----+-----+-----+-----+ 540
ACGGTGTGGAAACTCCTGAGGTTCTAGTACCAGAGACTGAAACCGGACAGGTTTTAAGT
A T P F E D S K I M V S D F G L S K I Q

FIG. 6A

541 AGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTCCT 600
-----+-----+-----+-----+-----+-----+
TCGACCGTTGTACGATCCGTGTGCGACACCCTGGGGTCTATACACCGGGGTCTCGAGGA
A G N M L G T A C G T P G Y V A P E L L

601 GGAGCAGAAACCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTACAT 660
-----+-----+-----+-----+-----+-----+
CCTCGTCTTTGGGATGCCCTTCCGGCATCTACACACCCGGGACCCACAGTAGAGGATGTA
E Q K P Y G K A V D V W A L G V I S Y I

661 CCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCAGAT 720
-----+-----+-----+-----+-----+-----+
GGACGACACACCCATGGGGGGGAAGATACTACTCTCGCTAGGACTTGAGAAGTCGGTCTA
L L C G Y P P F Y D E S D P E L F S Q I

721 TCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGACATCTCAGAATCAGCCAA 780
-----+-----+-----+-----+-----+-----+
AGACTCCCGGTGATGCTCAAACCTGAGAGGGAACCCCTACTGTAGAGTCTTAGTCGGTT
L R A S Y E F D S P F W D D I S E S A K

781 AGACTTCATTCCGGCACCTTCTGGAACGTGATCCCCAGAAGAGGTTACCTGCCAACAGGC 840
-----+-----+-----+-----+-----+-----+
TCTGAAGTAAGCCGTGGAAGACCTTGCACTAGGGGTCTTCTCCAAGTGGACGGTTGTCCG
D F I R H L L E R D P Q K R F T C Q Q A

841 CTTACAGCATCTCTGGATCTCTGGGGATGCAGCCTTGGACAGGGACATCCTAGGTTCTGT 900
-----+-----+-----+-----+-----+-----+
GAATGTCGTAGAGACCTAGAGACCCCTACGTCGGAACCTGTCCCTGTAGGATCCAAGACA
L Q H L W I S G D A A L D R D I L G S V

901 CAGTGAGCAGATCCAGAAGAATTTTGCCAGGACCCACTGGAAGCGTGCAATTCAATGCCAC 960
-----+-----+-----+-----+-----+-----+
GTCACCTCGTCTAGGTCTTCTTAAACGGTCTGCGGTGACCTTCGCACGTAAGTTACGGTG
S E Q I Q K N F A R T H W K R A F N A T

961 ATCATTCCTACGTACATCCGTAAGCTGGGACAGAGCCCAGAGGGTGAGGAGGCCTCCAG 1020
-----+-----+-----+-----+-----+-----+
TAGTAAGGATGCAGTGTAGGCATTGACCCCTGTCTCGGGTCTCCCACTCCTCCGGAGGTC
S F L R H I R K L G Q S P E G E E A S R

1021 GCAGGGTATGACCCGTCACAGCCACCCAGGCCTTGGGACTAGCCAGTCTCCCAAGTGGTG 1080
-----+-----+-----+-----+-----+-----+
CGTCCCATACTGGGCAGTGTGCGGTGGGTCCGGAACCCCTGATCGGTGAGAGGGTTACCAC
Q G M T R H S H P G L G T S Q S P K W V

FIG. 6B

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1081 ACAACCAGGTGGATGCCAAGGAAGGCCAAGTGGACTGACTCCTAGCTTTTCTTTCCTCCA 1140
-----+-----+-----+-----+-----+-----+
TGTGGTCCACCTACGGTTCCTTCCGGTTCACCTGACTGAGGATCGAAAAGAAAGGAGGT
T T R W M P R K A K W T D S

1141 GCCCTTTTGATCTCCTTCCCTGATCCTTGTCCTCCCGGACTGGCCTCTGTTGGAAAGTCCA 1200
-----+-----+-----+-----+-----+-----+
CGGGAAAAC TAGAGGAAGGGACTAGGAACAGGGGGCCTGACCGGAGACAACCTTTCAGGT

1201 AGACCGTGGGTGTGATGCATGGCACTGGGGTATGGGGCTTCCCAAGTATGTCCCCAGCCT 1260
-----+-----+-----+-----+-----+-----+
TCTGGCACCCACACTACGTACCGTGACCCCATACCCCGAAGGGTTCATACAGGGGTGCGA

1261 CTGTCCCTTTGTGCTGCCACCCCTCTATGGAACTGAGGAGGTATTCAAAAATGGATTTGG 1320
-----+-----+-----+-----+-----+-----+
GACAGGAAACAACGACGGTGGGAGATACCTTTGACTCCTCCATAAGTTTTACCTAAACC

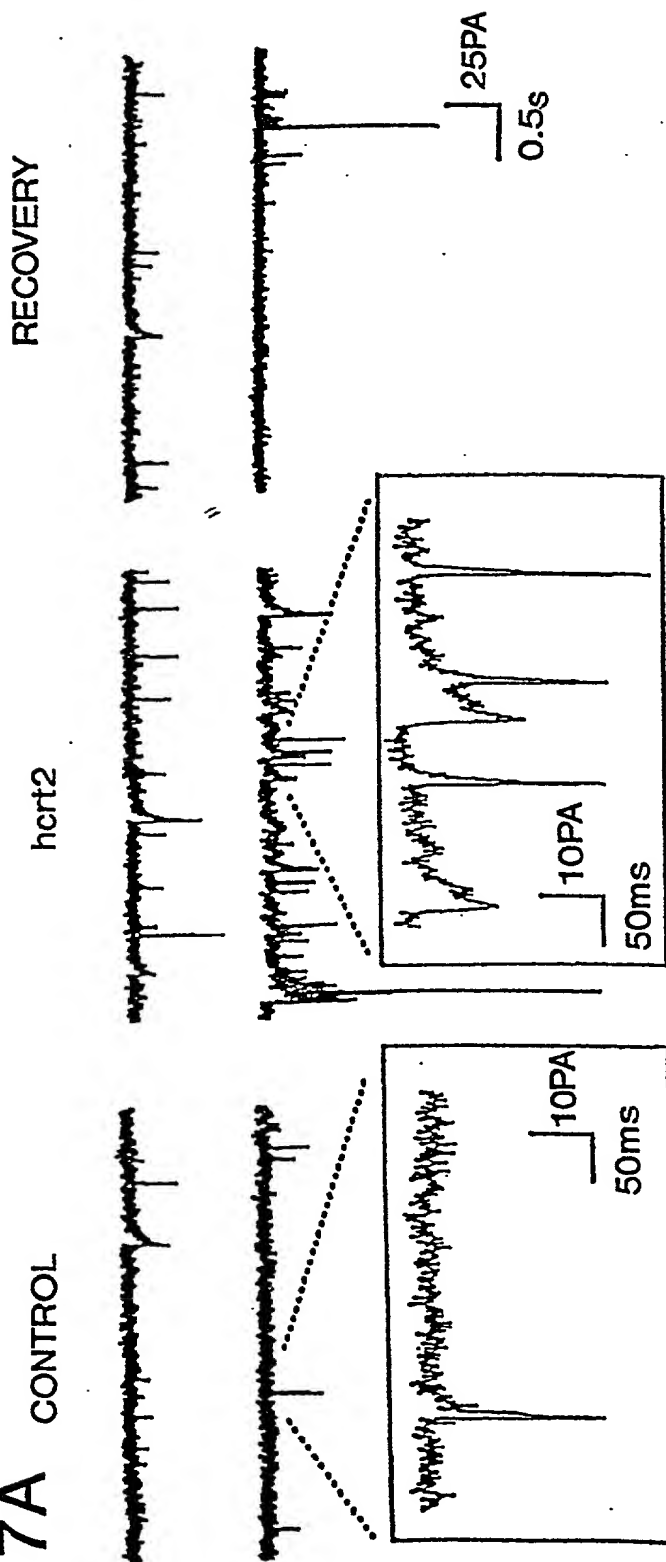
1321 GGGCCATCCTTCTGACCTTGACGACATATGCATTGCGTGGCTGTTCTGTGCTTTGC 1380
-----+-----+-----+-----+-----+-----+
CCCCGTAGGAAGGACGTGGAACGTGCGTGTATACGTAACGCACCGACAAGACACGAAACG

1381 TGA CTGTGGGTGGTCCTGCTTGTGTTGTAGCCCTTTAGTTCCTCCTCTTTCCAACCAATA 1440
-----+-----+-----+-----+-----+-----+
ACTGACACCCACCAGGACGAACACAACATCGGGAAATCAAGGAGGAGAAAGGTTGGTTAT

1441 AAGACAAACAGAACAAATG 1458
-----+-----
TTCTGTTTGTCTTGTTAC

FIG. 6C

FIG. 7A CONTROL



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FIG. 7B

